

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

RHEA

RRID:SCR_004713

Type: Tool

Proper Citation

RHEA (RRID:SCR_004713)

Resource Information

URL: <http://www.rhea-db.org/>

Proper Citation: RHEA (RRID:SCR_004713)

Description: Manually annotated reaction database where all reaction participants (reactants and products) are linked to the ChEBI database (Chemical Entities of Biological Interest) which provides detailed information about structure, formula and charge. Rhea provides built-in validations that ensure both elemental and charge balance of the reactions. The database has been populated with the reactions found in the Enzyme Commission (EC) list (and in the IntEnz and ENZYME databases), extending it with additional known reactions of biological interest. While the main focus of Rhea is enzyme-catalyzed reactions, other biochemical reactions are also included. Rhea is a manually annotated resource and it provides: stable reaction identifiers for each of its reactions; directionality information if the physiological direction of the reaction is known; the possibility to link several reactions together to form overall reactions; extensive cross-references to other resources including enzyme-catalyzed and other metabolic reactions, such as the EC list (in IntEnz), KEGG, MetaCyc and UniPathway; and chemical substructure and similarity searches on compounds in Rhea.

Abbreviations: RHEA

Resource Type: service resource, database, storage service resource, data repository, data or information resource

Defining Citation: [PMID:27789701](#)

Keywords: biochemical reaction, reaction, enzyme-catalyzed reaction, spontaneous reaction, enzyme, chemical reaction, gold standard, FASEB list

Funding: Swiss Federal Government SERI ;
SystemsX.ch ;
Swiss Initiative in Systems Biology ;
EMBL ;

European Union

Availability: Public, Free, Acknowledgement requested, Available for download, The community can contribute to this resource

Resource Name: RHEA

Resource ID: SCR_004713

Alternate IDs: r3d100010891, nlx_70986

Alternate URLs: <https://doi.org/10.17616/R3332H>

License: Creative Commons Attribution License

License URLs: <http://www.rhea-db.org/licensedisclaimer>

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260728T043206+0000

Ratings and Alerts

No rating or validation information has been found for RHEA.

No alerts have been found for RHEA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 172 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Luo Z, et al. (2025) Determinants of vacancy formation and migration in high-entropy alloys. Science advances, 11(1), eadr4697.

Tak??cs-Lov??sz K, et al. (2025) Altered aminoacid and lipid metabolism in a rat orofacial inflammation model determined by omics approach: potential role in trigeminal sensitisation. The journal of headache and pain, 26(1), 108.

Rashwan HH, et al. (2025) Insights into the tripartite relationship between cervical cancer, human papillomavirus, and the vaginal microbiome: a mega-analysis. Human genomics, 19(1), 89.

Pate SC, et al. (2025) RC-GNN: A predictive model of enzyme-reaction pairs. bioRxiv : the preprint server for biology.

Petraro S, et al. (2025) Plastic-Microbial BioRemediation DB: A Curated Database for Multi-Omics Applications. *Environmental microbiology reports*, 17(5), e70178.

Mou Y, et al. (2025) Outdoor air pollution, road traffic noise, and allostatic load in children aged 6-11 years: evidence from six European cohorts. *European journal of epidemiology*, 40(5), 537.

Gricourt G, et al. (2025) BioRGroup dataset: R-group expansion of ChEBI molecules referenced in the Rhea database. *Scientific data*, 12(1), 1692.

Zeng Z, et al. (2025) CLAIRE: a contrastive learning-based predictor for EC number of chemical reactions. *Journal of cheminformatics*, 17(1), 2.

Marzouk NH, et al. (2025) Proinflammatory and GABA eating bacteria in Parkinson's disease gut microbiome from a meta-analysis prospective. *NPJ Parkinson's disease*, 11(1), 145.

Kim GB, et al. (2025) Comprehensive evaluation of the capacities of microbial cell factories. *Nature communications*, 16(1), 2869.

Hutchison MG, et al. (2025) Evaluating User Experience and Satisfaction in a Concussion Rehabilitation App: Usability Study. *JMIR formative research*, 9, e67275.

Baumeister T, et al. (2025) Loss of FXR or Bile Acid-dependent Inhibition Accelerate Carcinogenesis of Gastroesophageal Adenocarcinoma. *Cellular and molecular gastroenterology and hepatology*, 19(8), 101505.

Coleman OI, et al. (2025) ATF6 activation alters colonic lipid metabolism causing tumour-associated microbial adaptation. *Nature metabolism*, 7(9), 1830.

Deng X, et al. (2025) Long-chain acyl-CoA synthetases: biological functions, diseases and therapeutic targets. *Molecular biomedicine*, 6(1), 117.

Haiman ZB, et al. (2025) RBC-GEM: A genome-scale metabolic model for systems biology of the human red blood cell. *PLoS computational biology*, 21(3), e1012109.

Intze E, et al. (2025) The infant microbiota hopscotches between community states toward maturation-longitudinal stool parameters and microbiota development in a cohort of European toddlers. *ISME communications*, 5(1), ycaf016.

Lv L, et al. (2025) A tunable and reversible thermo-inducible bio-switch for streptomycetes. *Nucleic acids research*, 53(2).

Ziegler FMR, et al. (2025) A full genome assembly reveals drought stress effects on gene expression and metabolite profiles in blackcurrant (*Ribes nigrum* L.). *Horticulture research*, 12(2), uhae313.

Jiang B, et al. (2025) Understanding disease-associated metabolic changes in human colonic epithelial cells using the iColonEpithelium metabolic reconstruction. *PLoS computational biology*, 21(7), e1013253.

Marston K, et al. (2025) Associations of family affluence with cortisol production and telomere length in European children. *EBioMedicine*, 117, 105793.